

Figure 1

trypsin: domain 1 of 1, from 217 to 443: score 293.0, E = 3.2e-92

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      *->IvGGreaqpgsfgsPwqvsIqvrsgggsrkhfCGGSLisenwVLTAA
      IvGG + ++ Pwq+slq+ + +h+CGGS+i + w++TAA
14094 217 IVGGNMSLLSQW--PWQASLQFQG-----YHLCGGSVITPLWIITAA 256

      HCvsgaasapassvrVSlsvrlGehnlsltegteqkfdvkktiivHpnyn
      HCv++ +++s+++ +G +sl + v+k i+ H++y
14094 257 HCVYD--LYLPKSWTI----QVGL--VSLLDNPAPSHLVEK-IVYHSKYK 297

      pdtldngaYdnDiAlLkLkspgvtlgdtrpicLpsassdlpvGttctvs
      p+ l+ nDiAl+kL++p +t+++ ++p+cLp + ++p+G c+ s
14094 298 PKRLG-----NDIALMKLAGP-LTFNEMIQPVCLPNSEENFPDGKVCWTS 341

      GwGrrptknlgl.sdtLqevvvpvvsretCrsayeyggtdDkvefvtdnm
      GwG t+++g+ s +L ++ vp++s+++ C+++ ygg +++ m
14094 342 GWGA--TEDGGdASPVLNHAAPPLISNKICNHRDVYGGI-----ISPSM 383

      iCagal.ggkdaCqGDSGGPLvcsgdnrdgrwelvGivSwGsygCargnk
      +Cag+l+gg+d+CqGDSGGPLvc w+lvG +S+G gCa+ nk
14094 384 LCAGYLTGGVDSCQGDSSGGPLVCQER---RLWKLVGATSFG-IGCAEVNK 429

      PGvytrVssyldWI<-*
      PGvytrV+s+ldWI
14094 430 PGVYTRVTSFLDWI 443

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Fig. 2A

trypsin\_2: domain 1 of 1, from 216 to 443: score 328.2, E = 9.2e-95

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      *->RIVGGseakigsfPWqvsLq.....CGGSLisprwVLTAAHC....
      RIVGG+ + ++PWq+sLq ++ + CGGS+I+p w++TAAHC +
14094 216 RIVGGNMSLLSQWPWQASLQfqqyhlCGGSVITPLWIITAAHCvydl 262

      .....rVrlGshdlssgeeteggprldspggqvikVskiievHpnYn..
      +++ ++ +G +l + + + V+ki+ H +Y ++
14094 263 ylpkswTIQVGLVSLLDNP-----APSHLVEKIV-YHSKYKpk 299

      ...NDIALLkLkepvtlstdsntvrPicLPssneiktsegntvpaGttctV
      + +NDIAL+kL+ p+t+++ ++P+cLP+s +++p+G c+
14094 300 rlgNDIALMKLAGPLTFNE--MIQPVCLPNS-----EENFPDGKVCWT 340

      sGWGrtsegpeesgggslpdvLqevnvpivsnetCr.....Ml
      sGWG t++ gg + vL ++ vp++sn+ C++++ +++ ++Ml
14094 341 SGWGATED-----GGDASPVLNHAAPPLISNKICNhrdvgyggiispsML 384

      CAGyleggntpgGkDaCqGDSGGPLvc.....vLvGiVSWGsssslygCa
      CAGyl+ gG+D+CqGDSGGPLvc++++ ++LvG +S+G +gCa
14094 385 CAGYLT-----GGVDSCQGDSSGGPLVCqerrlwKLVGATSFG----IGCA 425

      rpnkPGVYTrVssyldWI<-*
      + nkPGVYTrV+s+ldWI
14094 426 EVNKPVG YTRVTSFLDWI 443

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Fig. 2B

Fig. 3A

Begin SEQ ID NO 6

End SEQ ID NO 6

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*->stCggpdeFqCgsgrrCIprswvCDGdpDCeDGSDEslenCaa<-*
+C+ ++++C+s+ CI +CDG DC+DG+DE +C++
14094 71 FDGS--GKYRCRSSFKCIELIARCDGVSDCKDGEDE--YRCVR 109
  
```

Fig. 3B

Begin SEQ ID NO 7

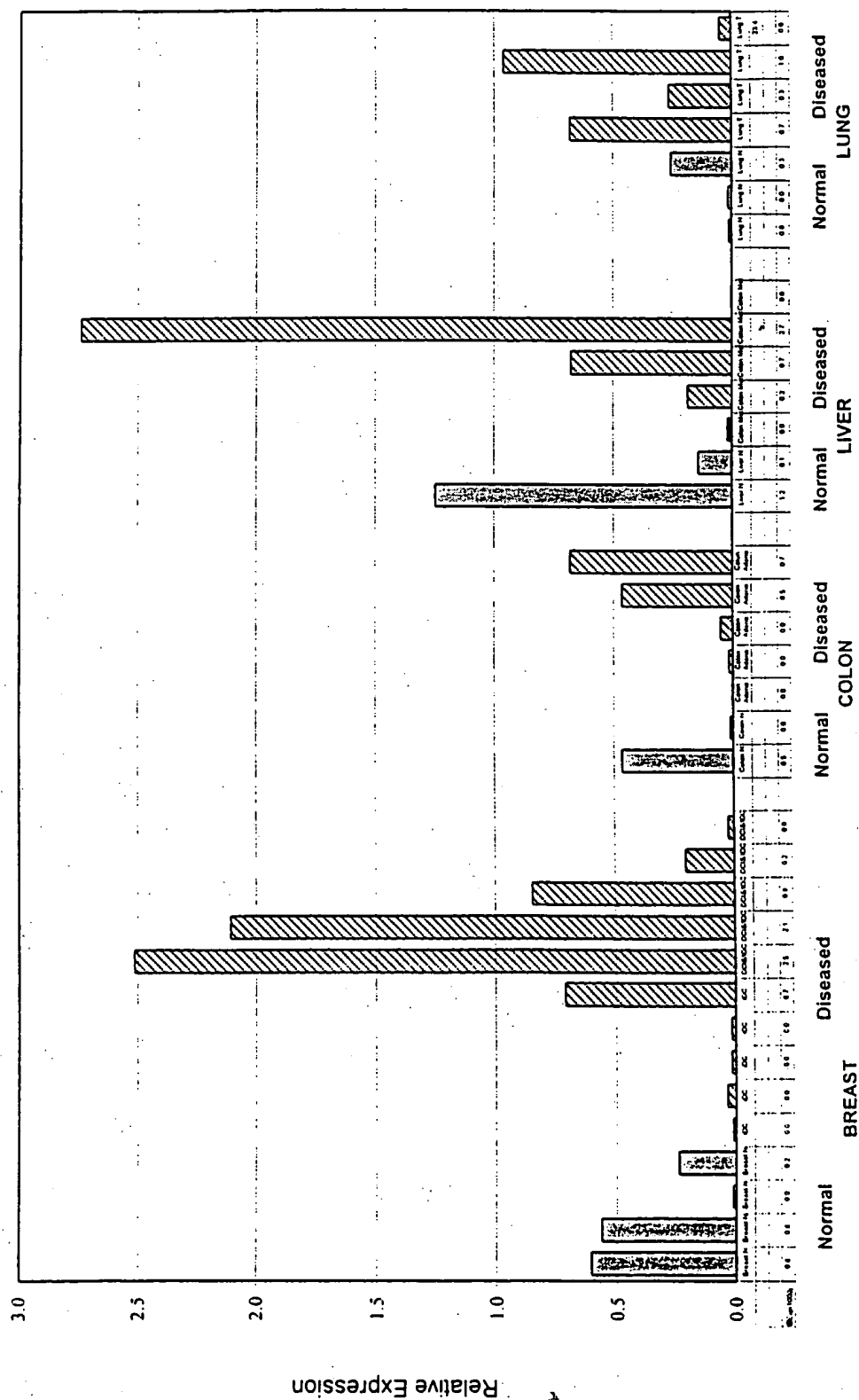
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*->vgGssrCeGrVEVrhgskWgtVCdssWslrdanvdpQaskvCrqLG
vgG +++ ++V+ + W+t C+++W + anv +C+qLG
14094 110 VGG--QNA-VLQVF-TAASWKTMCSDDWKGHYANV-----ACAQLG 146

CGgavsl1.gpyfsegggPagqreiwlbgvnCsGnE...tsLsqCpvrvt
+ vs+ + s+ g ++++++ ++++++ +++
14094 147 FPSYVSSDnLRVSSLEG-----QFREEFVSIHLLpdDKVTALHHS-- 187

ppglrqrqcsdhdgedagVvCs<-*
++ ++C g+ + ++C
14094 188 -VYVREGCAS-GHVVTLQCT 205
  
```

End SEQ ID NO 7



# 14094 Expression in Clinical Ovary Samples

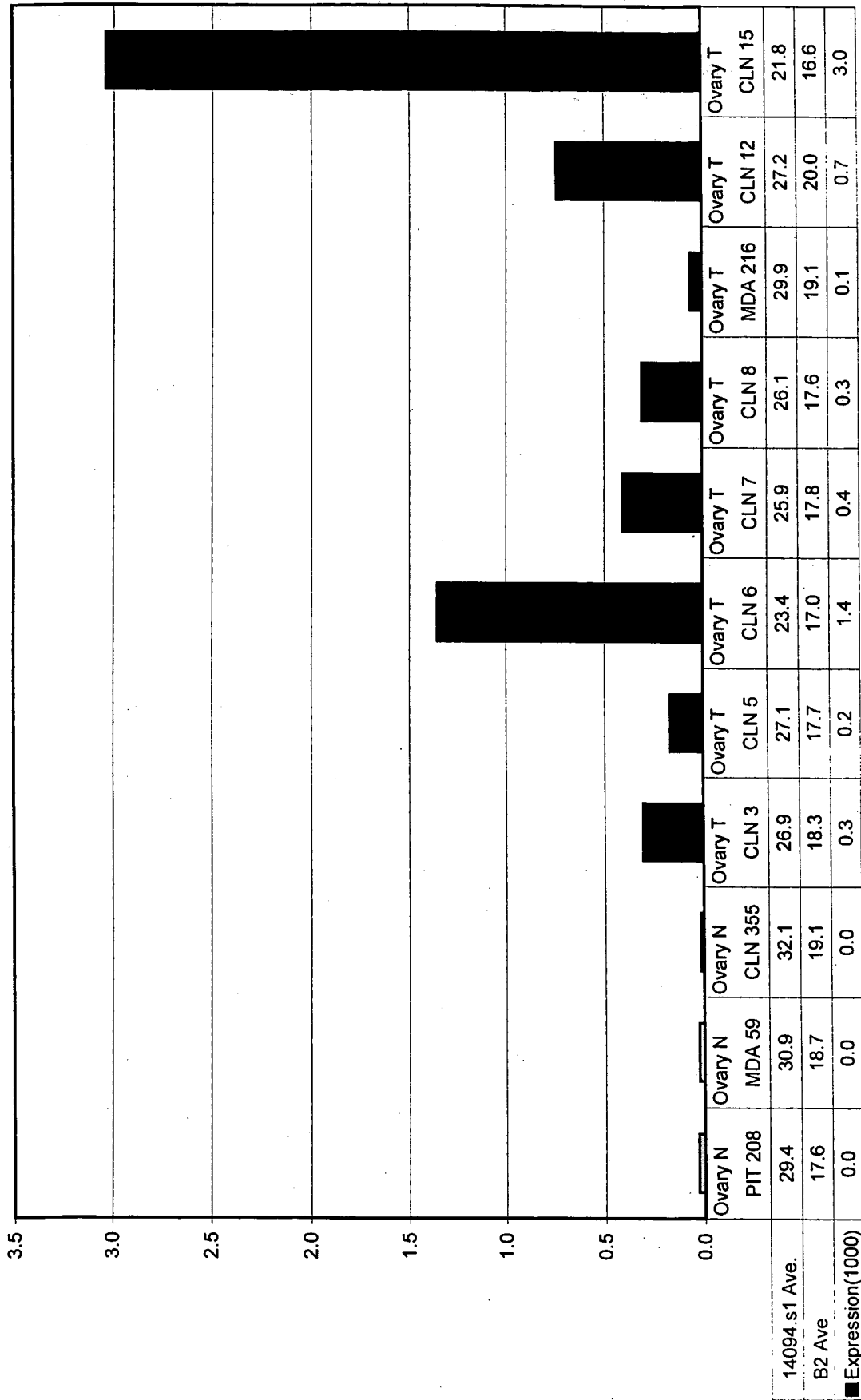


Figure 5

	MCF-7	ZR75	T47D	MDA 231	MDA 435	OLC-1	SW 460	SW 620	HCT 116	MT 20	Colo 205	NCIH 125	NCIH 69	NCIH 322	NCIH 480	A549	NHBE	MCF 10 MS	MCF 10A T c11	MCF 10A T c13	MCF 10A T36	MCF 10A T1	MCF 10C A12 c11
14084	26.7	30.0	25.6	27.2	30.5	22.5	25.6	23.7	32.7	26.1	24.2	31.2	26.0	31.6	32.4	32.0	31.4	26.1	32.3	32.1	31.2	31.2	32.2
82	20.6	21.6	21.1	19.0	17.6	21.7	19.8	21.3	21.1	19.1	18.0	20.3	21.7	21.4	20.1	21.9	20.6	20.5	19.9	19.9	20.0	20.2	17.4
Exp 11001	26.7	6.5	60.7	6.3	0.3	500	31.3	350.6	0.6	1.6	24.5	1.0	11.4	1.3	0.4	1.7	1.1	36.0	0.3	0.4	0.6	0.9	0.1

Fig. 6